

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/502,176

DATE: 03/06/2001
TIME: 12:22:41

Input Set : A:\ES.txt
Output Set: N:\CRF3\03062001\I502176.raw

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P#7 1642

of

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MAR 13 2001

TECH CENTER 1600/2900

3 <110> APPLICANT: Pirie-Shepherd, Steven
4 Folkman, M. Judah
6 <120> TITLE OF INVENTION: Deglycosylated Kringle 1-5 Region Fragments of Plasminogen and Methods
7 Use
9 <130> FILE REFERENCE: 05940-0141 (43171-219913)
11 <140> CURRENT APPLICATION NUMBER: US 09/502,176
12 <141> CURRENT FILING DATE: 2000-02-10
14 <150> PRIOR APPLICATION NUMBER: US 60/119,562
15 <151> PRIOR FILING DATE: 1999-02-10
17 <150> PRIOR APPLICATION NUMBER: US 60/128,062
18 <151> PRIOR FILING DATE: 1999-04-07
20 <160> NUMBER OF SEQ ID NOS: 2
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 780
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(780)
33 <400> SEQUENCE: 1
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35 Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly
36 1 5 10 15
38 acg atg tcc aaa aca aaa aat ggc atc acc tgt caa aaa tgg agt tcc 96
39 Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser
40 20 25 30
42 act tct ccc cac aga cct aga ttc tca cct gct aca cac ccc tca gag 144
43 Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu
44 35 40 45
46 gga ctg gag gag aac tac tgc agg aat cca gac aac gat ccg cag ggg 192
47 Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly
48 50 55 60
50 ccc tgg tgc tat act act gat cca gaa aag aga tat gac tac tgc gac 240
51 Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp
52 65 70 75 80
54 att ctt gag tgt gaa gag gaa tgt atg cat tgc agt gga gaa aac tat 288
55 Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr
56 85 90 95
58 gac ggc aaa att tcc aag acc atg tct gga ctg gaa tgc cag gcc tgg 336
59 Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp
60 100 105 110
62 gac tct cag agc cca cac gct cat gga tac att cct tcc aaa ttt cca 384
63 Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro
64 115 120 125
66 aac aag aac ctg aag aag aat tac tgt cgt aac ccc gat agg gag ctg 432
67 Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu

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68      130      135      140
70 cgg cct tgg tgt ttc acc acc gac ccc aac aag cgc tgg gaa ctt tgt      480
71 Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys
72 145      150      155      160
74 gac atc ccc cgc tgc aca aca cct cca cca tct tct ggt ccc acc tac      528
75 Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr Tyr
76      165      170      175
78 cag tgt ctg aag gga aca ggt gaa aac tat cgc ggg aat gtg gct gtt      576
79 Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val
80      180      185      190
82 acc gtg tcc ggg cac acc tgt cag cac tgg agt gca cag acc cct cac      624
83 Thr Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His
84      195      200      205
86 aca cat gaa agg aca cca gaa aac ttc ccc tgc aaa aat ttg gat gaa      672
87 Thr His Glu Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu
88      210      215      220
90 aac tac tgc cgc aat cct gac gga aaa agg gcc cca tgg tgc cat aca      720
91 Asn Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr
92 225      230      235      240
94 acc aac agc caa gtg cgg tgg gag tac tgt aag ata ccg tcc tgt gac      768
95 Thr Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys Asp
96      245      250      255
98 tcc tcc cca gta      780
99 Ser Ser Pro Val
100      260
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 260
105 <212> TYPE: PRT
106 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 2
110 Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly
111 1      5      10      15
114 Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser
115      20      25      30
118 Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu
119      35      40      45
122 Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly
123      50      55      60
126 Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp
127 65      70      75      80
130 Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr
131      85      90      95
134 Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp
135      100      105      110
138 Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro
139      115      120      125
142 Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu
143      130      135      140
146 Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys

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147 145          150          155          160
150 Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr Tyr
151          165          170          175
154 Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val
155          180          185          190
158 Thr Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His
159          195          200          205
162 Thr His Glu Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu
163 210          215          220
166 Asn Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr
167 225          230          235          240
170 Thr Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys Asp
171          245          250          255
174 Ser Ser Pro Val
175          260

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VERIFICATION SUMMARY

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